FIGURE

47 kDa protein sequence, noon Apr 15, 2003

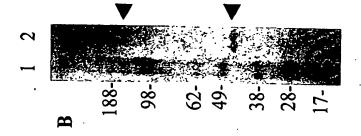
coverage (confirmed residues serine @S indicates acetylation of the N-terminal sednence Da) mass change +42.011 0/0 93 aa, MW 45936.94 average, 421 :**ෆ්** indicated in red). (yielding residue

@SDNGPQSNQR SAPRITFGGP TDSTDNNQNG GRNGARPKQR RPQGLPNNTA SWFTALTQHG KEELRFPRGQ GVPINTNSGP DDQIGYYRRA TRRVRGGDGK MKELSPRWYF YYLGTGPEAS PNNNAATVLQ LPQGTTLPKG FYAEGSRGGS ESKVSGKGQQ QTQGNFGDQD LIRQGTDYKH DKDPQFKDNV ILLNKHIDAY MSGASADSTO TVTLLPAADM DDFSRQLQNS LLLLDRLNQL GMEVTPSGTW LTYHGAIKLD ASGGGETALA TQAFGRRGPE TPKDHIGTRN SSRGNSPARM QQGQTVTKKS AAEASKKPRQ KRTATKQYNV PLPQRQKKQP VWVATEGALN RGNSRNSTPG DKKKKTDEAQ ASAFFGMSRI WPQIAQFAPS LPYGANKEGI KTEPPTEPKK QASSRSSSRS K 61 241 301 181 361 421

FIGURE 2

SARS protein 139 kDa

FIFLLFL TLTSGSDLDR CTTFDDVQAP NYTQHTSSMR GVYYPDEIFR SDTLYLTQDL FLPFYSNVTG FHTINHTFGN PVIPFKDGIY FAATEKSNVV RGWVFGSTMN NKSQSVIIIN NSTNVVIRAC NFELCONPFF AVSKPMGTQT HTMIFDNAFN CTFEYISDAF SLDVSEKSGN FKHLREFVFK NKDGFLYVYK GYQPIDVVRD LPSGFNTLKP IFKLPLGINI TNFRAILTAF SPAQDIWGTS AAAYFVGYLK PTTFMLKYDE NGTITDAVDC SQNPLAELKC SVKSFEIDKG IYQTSNFRVV PSGDVVRFPN ITNLCPFGEV FNATKFPSVY AWERKKISNC VADYSVLYNS TFFSTFKCYG VSATKLNDLC FSNVYADSFV VKGDDVRQIA PGQTGVIADY NYKLPDDFMG CVLAWNTRNI DATSTGNYNY KYRYLRHGKL RPFERDISNV PFSPDGKPCT PPALNCYWPL NDYGFYTTTG IGYQPYRVVV LSFELLNAPA TVCGPKLSTD LIKNQCVNFN FNGLTGTGVL TPSSKRFQPF QQFGRDVSDF TDSVRDPKTS EILDISPCAF GGVSVITPGT NASSEVAVLY QDVNCTDVST AIHADQLTPA WRIYSTGNNV FQTQAGCLIG AEHVDTSYEC DIPIGAGICA SYHTVSLLRS TSQKSIVAYT MSLGADSSIA YSNNTIAIPT NFSISITTEV MPVSMAKTSV DCNMYICGDS TECANLLLQY GSFCTQLNRA LSGIAAEQDR NTREVFAQVK QMYKTPTLKY FGGFNFSQIL PDPLKPTKRS FIEDLLFNKV TLADAGFMKQ YGECLGDINA RDLICAQKFN GLTVLPPLLT DDMIAAYTAA LVSGTATAGW TFGAGAALQI PFAMQMAYRF NGIGVTQNVL YENQKQIANQ FNKAISQIQE SLTTTSTALG KLQDVVNQNA QALNTLVKQL SSNFGAISSV LNDILSRLDK VEAEVQIDRL ITGRLQSLQT YVTQQLIRAA EIRASANLAA TKMSECVLGQ SKRVDFCGKG YHLMSFPQAA PHGVVFLHVT YVPSQERNFT TAPAICHEGK AYFPREGVFV FNGTSWFITQ RNFFSPQIIT TDNTFVSGNC DVVIGIINNT VYDPLQPELD SFKEELDKYF KNHTSPDVDL GDISGINASV VNIQKEIDRL NEVAKNLNES LIDLQELGKY EQYIKWPWYV WLGFIAGLIA IVMVTILLCC MTSCCSCLKG ACSCGSCCKF DEDDSEPVLK GVKLHYT



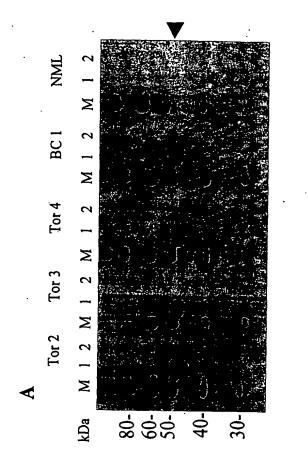
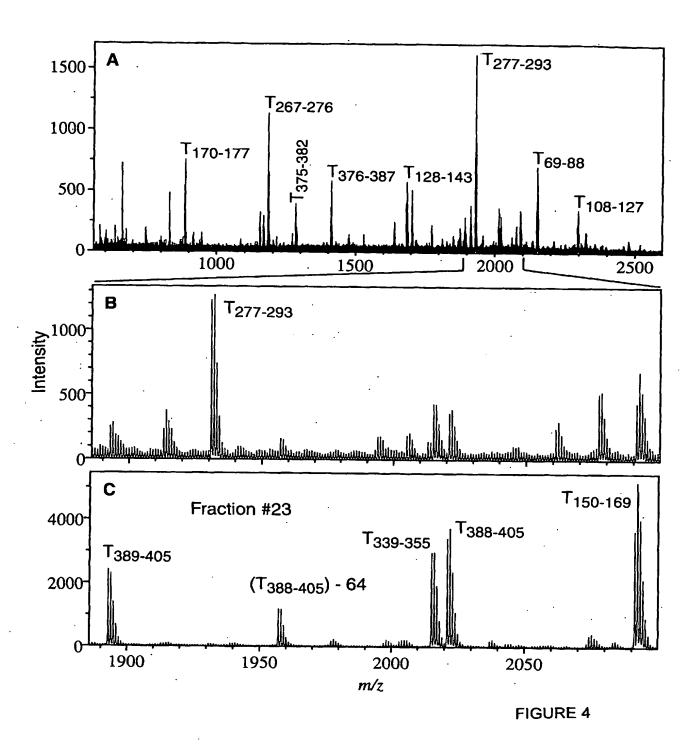


FIGURE 3



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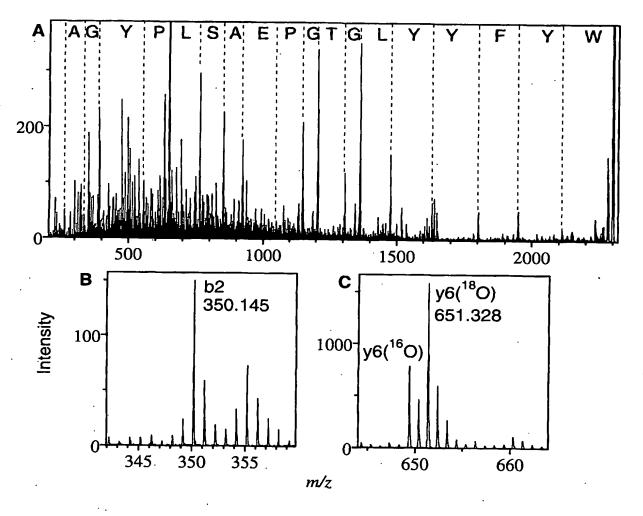
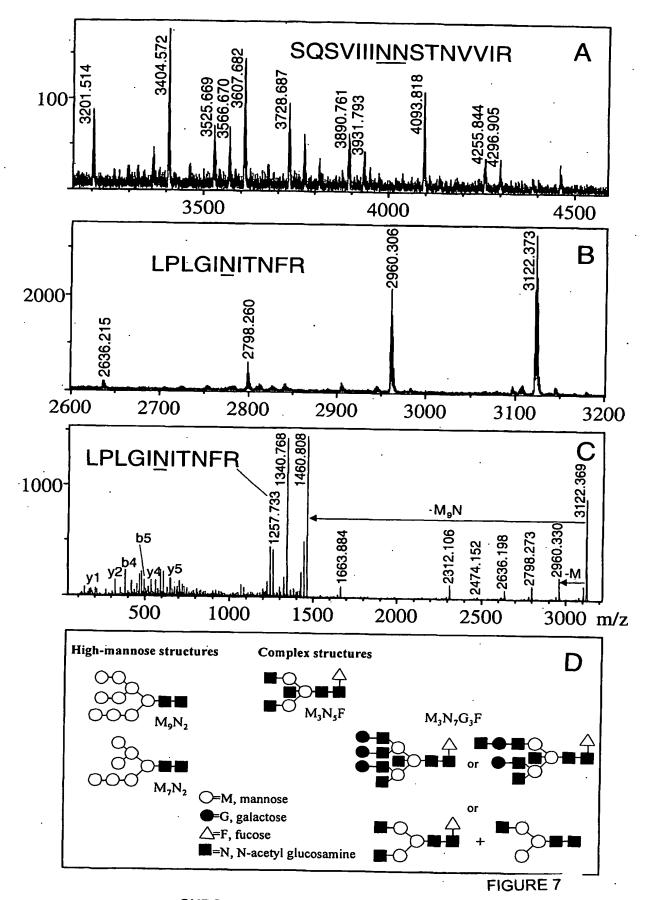


FIGURE 5

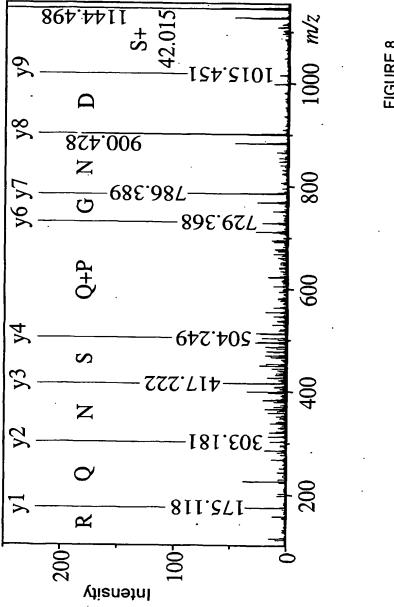
Coronavirus Nucleocapsid Protein Homology

	BERTHER TO THE STATE OF THE PARTY OF THE PAR	
• • •	WYFYYLGTGPEASLPYGAN	. SARS
• • •	WYFYYLGTGPHAKDQYGTD	. Human
	WYFYYLGTGPHAKDQYGTD	. Bovine
	WYFYYLGTGPHAKDQYGTD	. Turkey
	WYFYYLGTGPHAK <mark>H</mark> QYGTD	. Porcine
	WYFYYLGTGPHAK <mark>A</mark> QYGTN	. Equine
.• • •	WYFYYLGTGPHAGASYGDD	. Murine
• • •	WYFYYLGTGPHAGASFGDS	. Rat

FIGURE 6



SUBSTITUTE SHEET (RULE 26)



TDEAQPLPQR

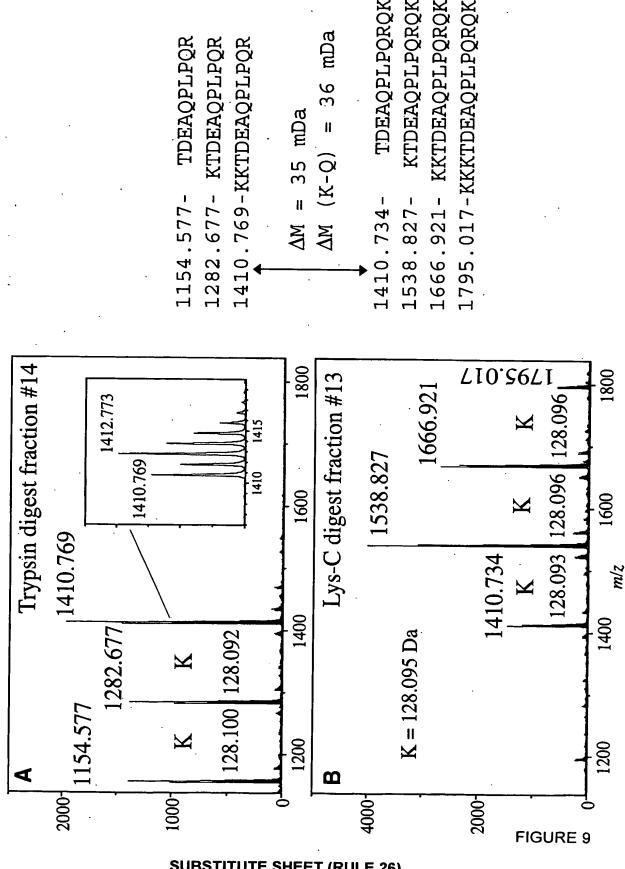
KTDEAQPLPQRQK

KKTDEAQPLPQRQK

TDEAQPLPQRQK

= 36 mDa

 $\Delta M = 35 \text{ mDa}$ $\Delta M \text{ (K-Q)} = 3$



SUBSTITUTE SHEET (RULE 26)

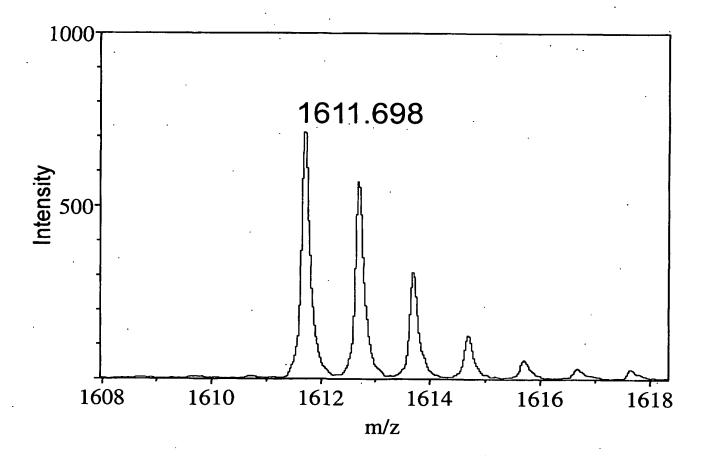


FIGURE 10

SWFTALTOHG YYLGTGPEAS FYAEGBREES ESKVSGKGQQ LIRQGTDYKH ILLNKHIDAY MSGASADSTQ RPOGLPNNTA MKELSPRWYF LPQGTTLPKG QTQGNFGDQD TVTLLPAADM DDFSRQLQNS LLLLDRLNQL LTYHGAIKLD DKDPQFKDNV SAPRITFGGP TDSTDNNQNG GRNGARPKQR TRRVRGGDGK PNNNAATVLO ASGGGETALA TQAFGRRGPE DDQIGYYRRA TPKDHIGTRN SSECNSPARM GMEVTPSGTW PLPQRQKKQP KRTATKOYNV GVPINTNSGP VWVATEGALN AAEASKKPRO KTFPPTEPKK DKKKKTDEAQ RENSENSTPG WPQIAQFAPS ASAFFGMSRI SDNGPQSNQR KEELRFPRGQ QQGQTVTKKS QAS<u>SRSS</u>SRE LPYGANKEGI 121 241 361 181 301 421

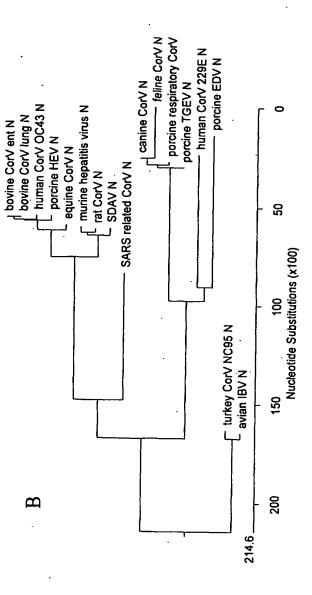


FIGURE 11

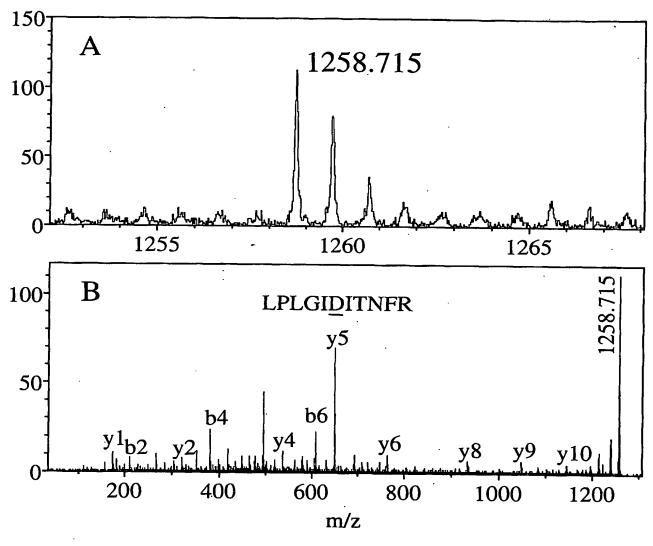


FIGURE 12